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(ii) TITLE OF THE INVENTION: VACCINE

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(iv) CORRESPONDENCE ADDRESS:

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(F) ZIP: TW8 9EP

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(C) OPERATING SYSTEM: DOS

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(vi) CURRENT APPLICATION DATA:

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(C) CLASSIFICATION:

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(B) FILING DATE:

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(C) REFERENCE/DOCKET NUMBER: B45124

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(C) TELEEX:

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(2) INFORMATION FOR SEQ ID NO:1:

(C) STRANDEDNESS: single

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Protein D 1/3 E7 his

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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[illegible]

65

Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val

50 55 60
 Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
 65 70 75 80
 Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
 85 90 95
 5 Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
 100 105 110
 Ala Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu
 115 120 125
 10 Gln Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser
 130 135 140
 Ser Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro
 145 150 155 160
 Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser
 165 170 175
 15 Thr Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu
 180 185 190
 Glu Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser
 195 200 205
 20 Gln Lys Pro Thr Ser Gly His His His His His
 210 215 220

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 663 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30 Protein D 1/3 E7 his

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

35 ATGGATCCAA GCAGCCATTC ATCAAATATG GCGAATACCC AAATGAAATC AGACAAAATC
 60 ATTATTGCTC ACCGTGGTGC TAGCGGTTAT TTACCAGAGC ATACGTTAGA ATCTAAAGCA
 120 CTTGCGTTTG CACAACAGGC TGATTATTTA GAGCAAGATT TAGCAATGAC TAAGGATGGT
 180 CGTTTAGTGG TTATTCACGA TCACTTTTTA GATGGCTTGA CTGATGTTGC GAAAAAATTC
 40 240 CCACATCGTC ATCGTAAAGA TGGCCGTTAC TATGTCATCG ACTTTACCTT AAAAGAAATT
 300 CAAAGTTTATG AAATGACAGA AACTTTTGAA ACCATGGCCA TGCATGGAGA TACACCTACA
 45 360 TTGCATGAAT ATATGTTAGA TTTGCAACCA GAGACAACTG ATCTCTACTG TTATGAGCAA
 420 TTAAATGACA GCTCAGAGGA GGAGGATGAA ATAGATGGTC CAGCTGGACA AGCAGAACCG
 480 GACAGAGCCC ATTACAATAT TGTAACCTTT TGTGCAAGT GTGACTCTAC GCTTCGGTTG
 50 540 TCGGTACAAA GCACACACGT AGACATTCGT ACTTTGGAAG ACCTGTTAAT GGGCACACTA
 600 GGAATTGTGT GCCCCATCTG TTCTCAGAAA CCAACTAGTG GCCACCATCA CCATCACCAT
 55 660 TAA
 663

(2) INFORMATION FOR SEQ ID NO:3:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 65 (D) TOPOLOGY: linear
 Protein D 1/3 E6 His/HPV 16

000290-92678660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5	60	ATGGATCCAA	GCAGCCATTC	ATCAAATATG	GCGAATACCC	AAATGAAATC	AGACAAAATC
	120	ATTATTGCTC	ACCGTGGTGC	TAGCGGTTAT	TTACCAGAGC	ATACGTTAGA	ATCTAAAGCA
	180	CTTGCGTTTG	CACAACAGGC	TGATTATTTA	GAGCAAGATT	TAGCAATGAC	TAAGGATGGT
10	240	CGTTTAGTGG	TTATTCACGA	TCACTTTTTA	GATGGCTTGA	CTGATGTTGC	GAAAAAATTC
	300	CCACATCGTC	ATCGTAAAGA	TGGCCGTTAC	TATGTGATCG	ACTTTACCTT	AAAAGAAATT
	360	CAAAGTTTAG	AAATGACAGA	AACTTTGAA	ACCATGGCCA	TGTTTCAGGA	CCCACAGGAG
15	420	CGACCCAGAA	AGTTACCACA	GTTATGCACA	GAGCTGCAAA	CAACTATACA	TGATATAATA
	480	TTAGAATGTG	TGTACTGCAA	GCAACAGTTA	CTGCGACGTG	AGGTATATGA	CTTTGCTTTT
20	540	CGGGATTTAT	GCATAGTATA	TAGAGATGGG	AATCCATATG	CTGTATGTGA	TAAATGTTTA
	600	AAGTTTTATT	CTAAAATTAG	TGAGTATAGA	CATTATTGTT	ATAGTTTGTA	TGGAACAACA
	660	TTAGAACAGC	AATACAACAA	ACCGTTGTGT	GATTTGTTAA	TTAGGTGTAT	TAAGTGTCAA
25	720	AAGCCACTGT	GTCCTGAAGA	AAAGCAAAGA	CATCTGGACA	AAAAGCAAAG	ATTCCATAAT
	780	ATAAGGGGTC	GGTGGACCGG	TCGATGTATG	TCTTGTTGCA	GATCATCAAG	AACACGTAGA
30	822	GAAACCCAGC	TGACTAGTGG	CCACCATCAC	CATCACCATT	AA	

(2) INFORMATION FOR SEQ ID NO: 4:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 274 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 40 Protein D 1/3 E6 His/HPV 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

45	Met	Asp	Pro	Ser	Ser	His	Ser	Ser	Asn	Met	Ala	Asn	Thr	Gln	Met	Lys
	1				5					10					15	
	Ser	Asp	Lys	Ile	Ile	Ile	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Leu	Pro
50				20					25					30		
	Glu	His	Thr	Leu	Glu	Ser	Lys	Ala	Leu	Ala	Phe	Ala	Gln	Gln	Ala	Asp
			35					40					45			
55	Tyr	Leu	Glu	Gln	Asp	Leu	Ala	Met	Thr	Lys	Asp	Gly	Arg	Leu	Val	Val
		50					55					60				
	Ile	His	Asp	His	Phe	Leu	Asp	Gly	Leu	Thr	Asp	Val	Ala	Lys	Lys	Phe
60	65				70							75				80
	Pro	His	Arg	His	Arg	Lys	Asp	Gly	Arg	Tyr	Tyr	Val	Ile	Asp	Phe	Thr
				85						90					95	
65	Leu	Lys	Glu	Ile	Gln	Ser	Leu	Glu	Met	Thr	Glu	Asn	Phe	Glu	Thr	Met
				100					105					110		
	Ala	Met	Phe	Gln	Asp	Pro	Gln	Glu	Arg	Pro	Arg	Lys	Leu	Pro	Gln	Leu
70			115					120					125			
	Cys	Thr	Glu	Leu	Gln	Thr	Thr	Ile	His	Asp	Ile	Ile	Leu	Glu	Cys	Val
		130					135					140				
75	Tyr	Cys	Lys	Gln	Gln	Leu	Leu	Arg	Arg	Glu	Val	Tyr	Asp	Phe	Ala	Phe
	145				150						155					160
	Arg	Asp	Leu	Cys	Ile	Val	Tyr	Arg	Asp	Gly	Asn	Pro	Tyr	Ala	Val	Cys
80				165						170					175	
	Asp	Lys	Cys	Leu	Lys	Phe	Tyr	Ser	Lys	Ile	Ser	Glu	Tyr	Arg	His	Tyr

180 190
Cys Tyr Ser Leu Tyr Gly Thr Thr Leu Glu Gln Gln Tyr Asn Lys Pro
195 200 205
Leu Cys Asp Leu Leu Ile Arg Cys Ile Asn Cys Gln Lys Pro Leu Cys
5 210 215 220
Pro Glu Glu Lys Gln Arg His Leu Asp Lys Lys Gln Arg Phe His Asn
225 230 235 240
Ile Arg Gly Arg Trp Thr Gly Arg Cys Met Ser Cys Cys Arg Ser Ser
245 250 255
10 Arg Thr Arg Arg Glu Thr Gln Leu Thr Ser Gly His His His His His
260 265 270
His

15 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
Protein D 1/3 E6/E7/ HPV16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

25 ATGGATCCAA GCAGCCATTC ATCAAATATG GCGAATACCC AAATGAAATC AGACAAAATC
60
ATTATTGCTC ACCGTGGTGC TAGCGGTTAT TTACCAGAGC ATACGTTAGA ATCTAAAGCA
120
30 CTTGCGTTTG CACAACAGGC TGATTATTTA GAGCAAGATT TAGCAATGAC TAAGGATGGT
180
CGTTTAGTGG TTATTCACGA TCACTTTTGA GATGGCTTGA CTGATGTTGC GAAAAAATTC
240
CCACATCGTC ATCGTAAAGA TGGCCGTTAC TATGTCATCG ACTTTACCTT AAAAGAAATT
35 300
CAAAGTTTAG AAATGACAGA AACTTTGAA ACCATGGCCA TGTTTCAGGA CCCACAGGAG
360
CGACCCAGAA AGTTACCACA GTTATGCACA GAGCTGCAA CAACTATACA TGATATAATA
420
40 TTAGAATGTG TGTACTGCAA GCAACAGTTA CTGCGAGGTG AGGTATATGA CTTTGCTTTT
480
CGGGATTTAT GCATAGTATA TAGAGATGGG AATCCATATG CTGTATGTGA TAAATGTTTA
540
AAGTTTTATT CTAAAATTAG TGAGTATAGA CATTATTGTT ATAGTTTGTA TGGAACAACA
45 600
TTAGAACAGC AATACAACAA ACCGTTGTGT GATTGTGTTA TTAGGTGTAT TAACTGTCAA
660
AAGCCACTGT GTCCTGAAGA AAAGCAAAGA CATCTGGACA AAAAGCAAAG ATTCCATAAT
720
50 ATAAGGGGTC GGTGGACCGG TCGATGTATG TCTTGTGCA GATCATCAAG AACACGTAGA
780
GAAACCCAGC TGATGCATGG AGATACACCT ACATTGCATG AATATATGTT AGATTTGCAA
840
CCAGAGACAA CTGATCTCTA CTGTTATGAG CAATTAAATG ACAGCTCAGA GGAGGAGGAT
55 900
GAAATAGATG GTCCAGCTGG ACAAGCAGAA CCGGACAGAG CCCATTACAA TATTGTAACC
960
TTTTGTGCA AGTGTGACTC TACGCTTCGG TTGTGCGTAC AAAGCACACA CGTAGACATT
1020
60 CGTACTTTGG AAGACCTGTT AATGGGCACA CTAGGAATTG TGTGCCCCAT CTGTTCTCAG
1080
AAACCAACTA GTGGCCACCA TCACCATCAC CATTAA
1116

65 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 Protein D 1/3 E6/E7/ HPV16

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

10 Met Asp Pro Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys
 1 5 10 15
 Ser Asp Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro
 20 25 30
 Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Ala Asp
 35 40 45
 15 Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
 50 55 60
 Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
 65 70 75 80
 20 Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
 85 90 95
 Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
 100 105 110
 25 Ala Met Phe Gln Asp Pro Gln Glu Arg Pro Arg Lys Leu Pro Gln Leu
 115 120 125
 Cys Thr Glu Leu Gln Thr Thr Ile His Asp Ile Ile Leu Glu Cys Val
 130 135 140
 Tyr Cys Lys Gln Gln Leu Leu Arg Arg Glu Val Tyr Asp Phe Ala Phe
 145 150 155 160
 30 Arg Asp Leu Cys Ile Val Tyr Arg Asp Gly Asn Pro Tyr Ala Val Cys
 165 170 175
 Asp Lys Cys Leu Lys Phe Tyr Ser Lys Ile Ser Glu Tyr Arg His Tyr
 180 185 190
 35 Cys Tyr Ser Leu Tyr Gly Thr Thr Leu Glu Gln Gln Tyr Asn Lys Pro
 195 200 205
 Leu Cys Asp Leu Leu Ile Arg Cys Ile Asn Cys Gln Lys Pro Leu Cys
 210 215 220
 Pro Glu Glu Lys Gln Arg His Leu Asp Lys Lys Gln Arg Phe His Asn
 225 230 235 240
 40 Ile Arg Gly Arg Trp Thr Gly Arg Cys Met Ser Cys Cys Arg Ser Ser
 245 250 255
 Arg Thr Arg Arg Glu Thr Gln Leu Met His Gly Asp Thr Pro Thr Leu
 260 265 270
 His Glu Tyr Met Leu Asp Leu Gln Pro Glu Thr Thr Asp Leu Tyr Cys
 275 280 285
 45 Tyr Glu Gln Leu Asn Asp Ser Ser Glu Glu Glu Asp Glu Ile Asp Gly
 290 295 300
 Pro Ala Gly Gln Ala Glu Pro Asp Arg Ala His Tyr Asn Ile Val Thr
 305 310 315 320
 50 Phe Cys Cys Lys Cys Asp Ser Thr Leu Arg Leu Cys Val Gln Ser Thr
 325 330 335
 His Val Asp Ile Arg Thr Leu Glu Asp Leu Leu Met Gly Thr Leu Gly
 340 345 350
 55 Ile Val Cys Pro Ile Cys Ser Gln Lys Pro Thr Ser Gly His His His
 355 360 365
 His His His
 370

(2) INFORMATION FOR SEQ ID NO:7:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 Protein D 1/3 E7 mutated HPV 16

65

00000 92618500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5 ATGGATCCAA GCAGCCATTC ATCAAATATG GCGAATACCC AAATGAAATC AGACAAAATC
 60 ATTATTGCTC ACCGTGGTGC TAGCGGTTAT TTAGCAGAGC ATACGTTAGA ATCTAAAGCA
 120 CTTGCGTTTG CACAACAGGC TGATTATTTA GAGCAAGATT TAGCAATGAC TAAGGATGGT
 180 CGTTTAGTGG TTATTCACGA TCACTTTTTA GATGGCTTGA CTGATGTTGC GAAAAAATTC
 240 CCACATCGTC ATCGTAAAGA TGGCCGTTAC TATGTCATCG ACTTTACCTT AAAAGAAATT
 300 CAAAGTTTAG AAATGACAGA AAACTTTGAA ACCATGGCCA TGCATGGAGA TACACCTACA
 15 360 TTGCATGAAT ATATGTTAGA TTTGCAACCA GAGACAACTG ATCTCTACGG TTATCAGCAA
 420 TTAAATGACA GCTCAGAGGA GGAGGATGAA ATAGATGGTC CAGCTGGACA AGCAGAACCG
 480 GACAGAGCCC ATTACAATAT TGTAACCTTT TGTGCAAGT GTGACTCTAC GCTTCGGTTG
 20 540 TCGGTACAAA GCACACACGT AGACATTCGT ACTTTGGAAG ACCTGTTAAT GGGCACACTA
 600 GGAATTGTGT GCCCCATCTG TTCTCAGAAA CCAACTAGTG GCCACCATCA CCATCACCAT
 25 660 TAA
 663

(2) INFORMATION FOR SEQ ID NO:8:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 35 (D) TOPOLOGY: linear

Protein D 1/3 E7 mutated HPV 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

40 Met Asp Pro Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys
 1 5 10 15
 Ser Asp Lys Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro
 20 25 30
 Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp
 45 35 40 45
 Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
 50 50 55 60
 Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
 65 70 75 80
 50 Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
 85 90 95
 Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
 100 105 110
 Ala Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu
 115 120 125
 55 Gln Pro Glu Thr Thr Asp Leu Tyr Gly Tyr Gln Gln Leu Asn Asp Ser
 130 135 140
 Ser Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro
 145 150 155 160
 60 Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser
 165 170 175
 Thr Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu
 180 185 190
 Glu Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser
 195 200 205
 65 Gln Lys Pro Thr Ser Gly His His His His His His

210

215

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(2) INFORMATION FOR SEQ ID NO:9:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 CLYTA E6 His HPV 16

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAAAGGGG GAATTGTACA TTCAGACGGC TCTTATCCAA AAGACAAGTT TGAGAAAATC
 15 60
 AATGGCACTT GGTACTACTT TGACAGTTCA GGCTATATGC TTGCAGACCG CTGGAGGAAG
 120
 CACACAGACG GCAACTGGTA CTGGTTCGAC AACTCAGGCG AAATGGCTAC AGGCTGGAAG
 180
 20 AAAATCGCTG ATAAGTGGTA CTATTTCAAC GAAGAAGGTG CCATGAAGAC AGGCTGGGTC
 240
 AAGTACAAGG ACACTTGGTA CTACTTAGAC GCTAAAGAAG GCGCCATGGT ATCAAATGCC
 300
 TTTATCCAGT CAGCGGACGG AACAGGCTGG TACTACCTCA AACCAGACGG AACACTGGCA
 25 360
 GACAGGCCAG AATTGGCCAG CATGCTGGAC ATGGGCATGT TTCAGGACCC ACAGGAGCGA
 420
 CCCAGAAAGT TACCACAGTT ATGCACAGAG CTGCAAACAA CTATACATGA TATAATATTA
 480
 30 GAATGTGTGT ACTGCAAGCA ACAGTTACTG CGACGTGAGG TATATGACTT TGCTTTTCGG
 540
 GATTTATGCA TAGTATATAG AGATGGGAAT CCATATGCTG TATGTGATAA ATGTTTAAAG
 600
 TTTTATTCTA AAATTAGTGA GTATAGACAT TATTGTTATA GTTTGTATGG AACAACTTA
 35 660
 GAACAGCAAT ACAACAAACC GTTGTGTGAT TTGTTAATTA GGTGTATTAA CTGTCAAAG
 720
 CCACTGTGTC CTGAAGAAAA GCAAAGACAT CTGGACAAAA AGCAAAGATT CCATAATATA
 780
 40 AGGGGTCGGT GGACCGGTCG ATGTATGTCT TGTGTCAGAT CATCAAGAAC ACGTAGAGAA
 840
 ACCCAGCTGA CTAGTGGCCA CCATCACCAT CACCATTAA
 879

45 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 CLYTA E6 His HPV 16

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

55

Met Lys Gly Gly Ile Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys
 1 5 10 15
 Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr
 20 25 30
 60 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
 35 40 45
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
 50 55 60
 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
 65 70 75 80
 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met

65

85 90 95
 Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr Tyr
 100 105 110
 5 Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Leu Ala Ser Met
 115 120 125
 Leu Asp Met Ala Met Phe Gln Asp Pro Gln Glu Arg Pro Arg Lys Leu
 130 135 140
 Pro Gln Leu Cys Thr Glu Leu Gln Thr Thr Ile His Asp Ile Ile Leu
 145 150 155 160
 10 Glu Cys Val Tyr Cys Lys Gln Gln Leu Leu Arg Arg Glu Val Tyr Asp
 165 170 175
 Phe Ala Phe Arg Asp Leu Cys Ile Val Tyr Arg Asp Gly Asn Pro Tyr
 180 185 190
 15 Ala Val Cys Asp Lys Cys Leu Lys Phe Tyr Ser Lys Ile Ser Glu Tyr
 195 200 205
 Arg His Tyr Cys Tyr Ser Leu Tyr Gly Thr Thr Leu Glu Gln Gln Tyr
 210 215 220
 Asn Lys Pro Leu Cys Asp Leu Leu Ile Arg Cys Ile Asn Cys Gln Lys
 225 230 235 240
 20 Pro Leu Cys Pro Glu Glu Lys Gln Arg His Leu Asp Lys Lys Gln Arg
 245 250 255
 Phe His Asn Ile Arg Gly Arg Trp Thr Gly Arg Cys Met Ser Cys Cys
 260 265 270
 25 Arg Ser Ser Arg Thr Arg Arg Glu Thr Gln Leu Thr Ser Gly His His
 275 280 285
 His His His His
 290

(2) INFORMATION FOR SEQ ID NO:11:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

CLYTA E7 HIS HPV 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

40 ATGAAAGGGG GAATTGTACA TTCAGACGGG TCTTATCCAA AAGACAAGTT TGAGAAAATC
 60 AATGGCACTT GGTACTACTT TGACAGTTCA GGCTATATGC TTGCAGACCG CTGGAGGAAG
 120 CACACAGACG GCAACTGGTA CTGGTTCGAC AACTCAGGCG AAATGGCTAC AGGCTGGAAG
 45 180 AAAATCGCTG ATAAGTGGTA CTATTTCAAC GAAGAAGGTG CCATGAAGAC AGGCTGGGTC
 240 AAGTACAAGG ACACTTGGTA CTA CTTAGAC GCTAAAGAAG GCGCCATGGT ATCAAATGCC
 300 TTTATCCAGT CAGCGGACGG AACAGGCTGG TACTACCTCA AACCAGACGG AACACTGGCA
 50 360 GACAGGCCAG AATTGGCCAG CATGCTGGAC ATGGCCATGC ATGGAGATAC ACCTACATTG
 420 CATGAATATA TGTTAGATTT GCAACCAGAG ACAACTGATC TCTACTGTTA TGAGCAATTA
 55 480 AATGACAGCT CAGAGGAGGA GGATGAAATA GATGGTCCAG CTGGACAAGC AGAACCGGAC
 540 AGAGCCCATT ACAATATTGT AACCTTTTGT TGCAAGTGTG ACTCTACGCT TCGGTTGTGC
 600 GTACAAAGCA CACACGTAGA CATTCTGACT TTGGAAGACC TGTTAATGGG CACACTAGGA
 660 ATTGTGTGCC CCATCTGTTC TCAGAAACCA ACTAGTGGCC ACCATCACCA TCACCATTAA
 720

65

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 CLYTA E7 HIS HPV 16

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

10 Met Lys Gly Gly Ile Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys
 1 5 10 15
 Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr
 20 25 30
 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
 15 35 40 45
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
 50 55 60
 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
 65 70 75 80
 20 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
 85 90 95
 Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr Tyr
 100 105 110
 Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Leu Ala Ser Met
 115 120 125
 25 Leu Asp Met Ala Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met
 130 135 140
 Leu Asp Leu Gln Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu
 145 150 155 160
 30 Asn Asp Ser Ser Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln
 165 170 175
 Ala Glu Pro Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys
 180 185 190
 Cys Asp Ser Thr Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile
 195 200 205
 35 Arg Thr Leu Glu Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro
 210 215 220
 Ile Cys Ser Gln Lys Pro Thr Ser Gly His His His His His His
 225 230 235

40

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 CLYTA E6E7 His HPV16

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

50 ATGAAAGGGG GAATTGTACA TTCAGACGGC TCTTATCCAA AAGACAAGTT TGAGAAAATC
 60 AATGGCACTT GGTACTACTT TGACAGTICA GGCTATATGC TTGCAGACCG CTGGAGGAAG
 55 120 CACACAGACG GCAACTGGTA CTGGTTGGAC AACTCAGGCG AAATGGCTAC AGGCTGGAAG
 180 AAAATCGCTG ATAAGTGGTA CTATTTCAAC GAAGAAGGTG CCATGAAGAC AGGCTGGGTC
 240 AAGTACAAGG ACACTTGGTA CTA CTAGAC GCTAAAGAAG GCGCCATGGT ATCAAATGCC
 60 300 TTTATCCAGT CAGCGGACGG AACAGGCTGG TACTACCTCA AACCAGACGG AACACTGGCA
 360 GACAGGCCAG AATTGGCCAG CATGCTGGAC ATGGCCATGT TTCAGGACCC ACAGGAGCGA
 65 420

	480	CCCAGAAAGT	TACCACAGTT	ATGCACAGAG	CTGCAAAACAA	CTATACATGA	TATAATATTA
	540	GAATGTGTGT	ACTGCAAGCA	ACAGTTACTG	CGAGGTGAGG	TATATGACTT	TGCTTTTCGG
5	600	GATTTATGCA	TAGTATATAG	AGATGGGAAT	CCATATGCTG	TATGTGATAA	ATGTTTAAAG
	660	TTTTATTCTA	AAATTAGTGA	GTATAGACAT	TATTGTTATA	GTTTGTATGG	AACAACATTA
	720	GAACAGCAAT	ACAACAAACC	GTTGTGTGAT	TTGTTAATTA	GGTGTATTAA	CTGTCAAAAG
10	780	CCACTGTGTC	CTGAAGAAAA	GCAAAGACAT	CTGGACAAAA	AGCAAAGATT	CCATAATATA
	840	AGGGGTCGGT	GGACCGGTCT	ATGTATGTCT	TGTTGCAGAT	CATCAAGAAC	ACGTAGAGAA
15	900	ACCCAGCTGA	TGCATGGAGA	TACACCTACA	TTGCATGAAT	ATATGTTAGA	TTTGCAACCA
	960	GAGACAACCT	ATCTCTACTG	TTATGAGCAA	TTAAATGACA	GCTCAGAGGA	GGAGGATGAA
	1020	ATAGATGGTC	CAGCTGGACA	AGCAGAACCG	GACAGAGCCC	ATTACAATAT	TGTAACCTTT
20	1080	TGTTGCAAGT	GTGACTCTAC	GCTTCGGTTG	TGCGTACAAA	GCACACACGT	AGACATTTCG
	1140	ACTTTGGAAG	ACCTGTTAAT	GGGCACACTA	GGAATTGTGT	GCCCCATCTG	TTCTCAGAAA
25	1173	CCAAC TAGTG	GCCACCATCA	CCATCACCAT	TAA		

(2) INFORMATION FOR SEQ ID NO:14:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 35 CLYTA E6E7 His HPV16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

40	Met	Lys	Gly	Gly	Ile	Val	His	Ser	Asp	Gly	Ser	Tyr	Pro	Lys	Asp	Lys
	1				5					10					15	
	Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser	Ser	Gly	Tyr
45	Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	Tyr	Trp
			20						25					30		
			35					40						45		
50	Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	Ala	Asp
	50						55					60				
	Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	Trp	Val
55	Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	Ala	Met
	65				70					75					80	
					85					90					95	
60	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr	Tyr
				100					105					110		
	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Leu	Ala	Ser	Met
65	Leu	Asp	Met	Ala	Met	Phe	Gln	Asp	Pro	Gln	Glu	Arg	Pro	Arg	Lys	Leu
	130						135					140				
	Pro	Gln	Leu	Cys	Thr	Glu	Leu	Gln	Thr	Thr	Ile	His	Asp	Ile	Ile	Leu
70	Glu	Cys	Val	Tyr	Cys	Lys	Gln	Gln	Leu	Leu	Arg	Arg	Glu	Val	Tyr	Asp
	145				150					155					160	
					165					170					175	
75	Phe	Ala	Phe	Arg	Asp	Leu	Cys	Ile	Val	Tyr	Arg	Asp	Gly	Asn	Pro	Tyr
				180					185					190		
	Ala	Val	Cys	Asp	Lys	Cys	Leu	Lys	Phe	Tyr	Ser	Lys	Ile	Ser	Glu	Tyr
80	Arg	His	Tyr	Cys	Tyr	Ser	Leu	Tyr	Gly	Thr	Thr	Leu	Glu	Gln	Gln	Tyr
	195						200					205				
							210					220				

[illegible]

(2) INFORMATION FOR SEQ ID NO:15:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- Protein D 1/3 E7 his HPV 18

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

35

35	ATGGATCCAA	GCAGCCATTC	ATCAAATATG	GCGAATACCC	AAATGAAATC	AGACAAAATC
60	ATTATTGCTC	ACCGTGGTGC	TAGCGGTTAT	TTACCAGAGC	ATACGTTAGA	ATCTAAAGCA
120	CTTGCGTTTG	CACAACAGGC	TGATTATTTA	GAGCAAGATT	TAGCAATGAC	TAAGGATGGT
40	180	CGTTTAGTGG	TTATTCACGA	TCACTTTITA	GATGGCTTGA	CTGATGTTGC
240	CCACATCGTC	ATCGTAAAGA	TGGCCGTAC	TATGTCATCG	ACTTTACCTT	AAAAGAAATT
45	300	CAAAGTTTAG	AAATGACAGA	AAACTTTGAA	ACCATGGCCA	TGCATGGACC
360	TTGCAAGACA	TTGTATTGCA	TTTAGAGCCC	CAAAATGAAA	TTCCGGTTGA	CCTTCTATGT
420	CACGAGCAAT	TAAGCGACTC	AGAGGAAGAA	AACGATGAAA	TAGATGAAGT	TAATCATCAA
50	480	CATTTACCAG	CCCGACGAGC	CGAACCACAA	CGTCACACAA	TGTTGTGTAT
540	TGTGAAGCCA	GAATTGAGCT	AGTAGTAGAA	AGCTCAGCAG	ACGACCTTCG	AGCATTCCAG
55	600	CAGCTGTTTT	TGAACACCCT	GTCCTTTGTG	TGTCCGTGGT	GTGCATCCCA
660	GGCCACCATC	ACCATCACCA	TTAA			
684						

60

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

[illegible]

(2) INFORMATION FOR SEQ ID NO:17:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
Thioredoxin

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

	Met	Ser	Asp	Lys	Ile	Ile	His	Leu	Thr	Asp	Asp	Ser	Phe	Asp	Thr	Asp
	1				5					10					15	
50	Val	Leu	Lys	Ala	Asp	Gly	Ala	Ile	Leu	Val	Asp	Phe	Trp	Ala	Glu	Trp
				20					25					30		
	Cys	Gly	Pro	Cys	Lys	Met	Ile	Ala	Pro	Ile	Leu	Asp	Glu	Ile	Ala	Asp
			35					40					45			
	Glu	Tyr	Gln	Gly	Lys	Leu	Thr	Val	Ala	Lys	Leu	Asn	Ile	Asp	Gln	Asn
55		50					55					60				
	Pro	Gly	Thr	Ala	Pro	Lys	Tyr	Gly	Ile	Arg	Gly	Ile	Pro	Thr	Leu	Leu
	65					70					75					80
	Leu	Phe	Lys	Asn	Gly	Glu	Val	Ala	Ala	Thr	Lys	Val	Gly	Ala	Leu	Ser
				85						90					95	
60	Lys	Gly	Gln	Leu	Lys	Glu	Phe	Leu	Asp	Ala	Asn	Leu	Ala			
				100					105							

(2) INFORMATION FOR SEQ ID NO:18:

65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 684 base pairs

5

	60	ATGGATCCAA	GCAGCCATTC	ATCAAATATG	GCGAATACCC	AAATGAAATC	AGACAAAATC
10	120	ATTATTGCTC	ACCGTGGTGC	TAGCGGTTAT	TTACCAGAGC	ATACGTTAGA	ATCTAAAGCA
	180	CTTGCGTTTG	CACAACAGGC	TGATTATTTA	GAGCAAGATT	TAGCAATGAC	TAAGGATGGT
	240	CGTTTAGTGG	TTATTCACGA	TCACTTTTTA	GATGGCTTGA	CTGATGTTGC	GAAAAAATTC
15	300	CCACATCGTC	ATCGTAAAGA	TGGCCGTTAC	TATGTCATCG	ACTTTACCTT	AAAAGAAATT
	360	CAAAGTTTAG	AAATGACAGA	AACTTTGAA	ACCATGGCCA	TGCATGGACC	TAAGGCAACA
20	420	TTGCAAGACA	TTGTATTGCA	TTTAGAGCCC	CAAAATGAAA	TTCCGTTTGA	CCTTCTAGGT
	480	CACCAGCAAT	TAAGCGACTC	AGAGGAAGAA	AACGATGAAA	TAGATGGAGT	TAATCATCAA
	540	CATTTACCAG	CCCGACGAGC	CGAACCACAA	CGTCACACAA	TGTTGTGTAT	GTGTTGTAAG
25	600	TGTGAAGCCA	GAATTGAGCT	AGTAGTAGAA	AGCTCAGCAG	ACGACCTTCG	AGCATTCCAG
	660	CAGCTGTTTC	TGAACACCCT	GTCCTTTGTG	TGTCCGTGGT	GTGCATCCCA	GCAGACTAGT
30	684	GGCCACCATC	ACCATCACCA	TTAA			

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

45	Met	Asp	Pro	Ser	Ser	His	Ser	Ser	Asn	Met	Ala	Asn	Thr	Gln	Met	Lys
	1			5					10					15		
	Ser	Asp	Lys	Ile	Ile	Ile	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Leu	Pro
			20						25					30		
	Glu	His	Thr	Leu	Glu	Ser	Lys	Ala	Leu	Ala	Phe	Ala	Gln	Gln	Ala	Asp
50			35					40					45			
	Tyr	Leu	Glu	Gln	Asp	Leu	Ala	Met	Thr	Lys	Asp	Gly	Arg	Leu	Val	Val
		50					55					60				
	Ile	His	Asp	His	Phe	Leu	Asp	Gly	Leu	Thr	Asp	Val	Ala	Lys	Lys	Phe
	65				70						75					80
55	Pro	His	Arg	His	Arg	Lys	Asp	Gly	Arg	Tyr	Tyr	Val	Ile	Asp	Phe	Thr
				85						90					95	
	Leu	Lys	Glu	Ile	Gln	Ser	Leu	Glu	Met	Thr	Glu	Asn	Phe	Glu	Thr	Met
			100						105					110		
	Ala	Met	His	Gly	Pro	Lys	Ala	Thr	Leu	Gln	Asp	Ile	Val	Leu	His	Leu
60			115					120					125			
	Glu	Pro	Gln	Asn	Glu	Ile	Pro	Val	Asp	Leu	Leu	Gly	His	Gln	Gln	Leu
		130					135					140				
	Ser	Asp	Ser	Glu	Glu	Glu	Asn	Asp	Glu	Ile	Asp	Gly	Val	Asn	His	Gln
	145					150					155					160
65	His	Leu	Pro	Ala	Arg	Arg	Ala	Glu	Pro	Gln	Arg	His	Thr	Met	Leu	Cys
				165						170					175	

10 (2) INFORMATION FOR SEQ ID NO:20:

15

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

50 (2) INFORMATION FOR SEQ ID NO:21:

55

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

60	Met	Asp	Pro	Ser	Ser	His	Ser	Ser	Asn	Met	Ala	Asn	Thr	Gln	Met	Lys
	1				5					10					15	
	Ser	Asp	Lys	Ile	Ile	Ile	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Leu	Pro
			20						25					30		
65	Glu	His	Thr	Leu	Glu	Ser	Lys	Ala	Leu	Ala	Phe	Ala	Gln	Ala	Asp	
			35					40					45			

	ATGGATCCAA	GCAGCCATTC	ATCAAATATG	GCGAATACCC	AAATGAAATC	AGACAAAATC
45	60	ATTATTGCTC	ACCGTGGTGC	TAGCGGTTAT	TTACCAGAGC	ATACGTTAGA
	120	CTTGCGTTTG	CACAACAGGC	TGATTATTTA	GAGCAAGATT	TAGCAATGAC
	180	CGTTTGTAGG	TTATTCACGA	TCACCTTTTA	GATGGCTTGA	CTGATGTTGC
50	240	CCACATCGTC	ATCGTAAAGA	TGGCCGTTAC	TATGTCATCG	ACTTTACCTT
	300	CAAAGTTTAG	AAATGACAGA	AAACTTTGAA	ACCATGGCGC	GCTTTGAGGA
	360	CGACCCTACA	AGCTACCTGA	TCTGTGCACG	GAACTGAACA	CTTCACTGCA
55	420	ATAACCTGTG	TATATTGCAA	GACAGTATTG	GAACTTACAG	AGGTATTTGA
	480	AAAGATTTAT	TTGTGGTGTA	TAGAGACAGT	ATACCGCATG	CTGCATGCCA
60	540	GATTTTTATT	CTAGAATTAG	AGAATTAAGA	CATTATTCAG	ACTCTGTGTA
	600	TTGGAAAAAC	TAACCTAACAC	TGGGTTATAC	AATTTATTAA	TAAGGTGCCT
	660	AAACCGTTGA	ATCCAGCAGA	AAACTTAGA	CACCTTAATG	AAAAACGACG
65	720					ATTTCAACA

[illegible]

ATAGCTGGGC ACTATAGAGG CCAAGTGGCAT TCGTGCTGCA ACCGAGCAGC ACAGGAACGA
 780
 CTCCAACGAC GCAGAGAAAC ACAAGTAATG CATGGACCTA AGGCAACATT GCAAGACATT
 840
 5 GTATTGCATT TAGAGCCCCA AAATGAAATT CCGGTTGACC TTCTATGTCA CGAGCAATTA
 900
 AGCGACTCAG AGGAAGAAAA CGATGAAATA GATGGAGTTA ATCATCAACA TTTACCAGCC
 960
 CGACGAGCCG AACCACAACG TCACACAATG TTGTGTATGT GTTGTAAAGTG TGAAGCCAGA
 1020
 10 ATTGAGCTAG TAGTAGAAAG CTCAGCAGAC GACCTTCGAG CATTCCAGCA GCTGTTTCTG
 1080
 AACACCCTGT CCTTTGTGTG TCCGTGGTGT GCATCCCAGC AGACTAGTGG CCACCATCAC
 1140
 15 CATCACCATT AA
 1152

(2) INFORMATION FOR SEQ ID NO:23:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 25 Protein D1/3 E6 E7 His/ HPV 18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

30	Met	Asp	Pro	Ser	Ser	His	Ser	Ser	Asn	Met	Ala	Asn	Thr	Gln	Met	Lys
	1				5					10					15	
	Ser	Asp	Lys	Ile	Ile	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Leu	Pro	
			20					25					30			
	Glu	His	Thr	Leu	Glu	Ser	Lys	Ala	Leu	Ala	Phe	Ala	Gln	Gln	Ala	Asp
			35					40					45			
35	Tyr	Leu	Glu	Gln	Asp	Leu	Ala	Met	Thr	Lys	Asp	Gly	Arg	Leu	Val	Val
		50					55					60				
	Ile	His	Asp	His	Phe	Leu	Asp	Gly	Leu	Thr	Asp	Val	Ala	Lys	Lys	Phe
	65					70					75					80
	Pro	His	Arg	His	Arg	Lys	Asp	Gly	Arg	Tyr	Tyr	Val	Ile	Asp	Phe	Thr
				85						90					95	
40	Leu	Lys	Glu	Ile	Gln	Ser	Leu	Glu	Met	Thr	Glu	Asn	Phe	Glu	Thr	Met
				100					105					110		
	Ala	Arg	Phe	Glu	Asp	Pro	Thr	Arg	Arg	Pro	Tyr	Lys	Leu	Pro	Asp	Leu
				115				120					125			
45	Cys	Thr	Glu	Leu	Asn	Thr	Ser	Leu	Gln	Asp	Ile	Glu	Ile	Thr	Cys	Val
		130					135					140				
	Tyr	Cys	Lys	Thr	Val	Leu	Glu	Leu	Thr	Glu	Val	Phe	Glu	Phe	Ala	Phe
	145					150					155					160
	Lys	Asp	Leu	Phe	Val	Val	Tyr	Arg	Asp	Ser	Ile	Pro	His	Ala	Ala	Cys
				165						170					175	
50	His	Lys	Cys	Ile	Asp	Phe	Tyr	Ser	Arg	Ile	Arg	Glu	Leu	Arg	His	Tyr
				180					185					190		
	Ser	Asp	Ser	Val	Tyr	Gly	Asp	Thr	Leu	Glu	Lys	Leu	Thr	Asn	Thr	Gly
			195					200					205			
55	Leu	Tyr	Asn	Leu	Leu	Ile	Arg	Cys	Leu	Arg	Cys	Gln	Lys	Pro	Leu	Asn
		210					215					220				
	Pro	Ala	Glu	Lys	Leu	Arg	His	Leu	Asn	Glu	Lys	Arg	Arg	Phe	His	Asn
	225					230					235					240
	Ile	Ala	Gly	His	Tyr	Arg	Gly	Gln	Cys	His	Ser	Cys	Cys	Asn	Arg	Ala
				245						250					255	
60	Arg	Gln	Glu	Arg	Leu	Gln	Arg	Arg	Arg	Glu	Thr	Gln	Val	Met	His	Gly
				260					265					270		
	Pro	Lys	Ala	Thr	Leu	Gln	Asp	Ile	Val	Leu	His	Leu	Glu	Pro	Gln	Asn
			275					280					285			
65	Glu	Ile	Pro	Val	Asp	Leu	Leu	Cys	His	Glu	Gln	Leu	Ser	Asp	Ser	Glu
		290					295					300				

